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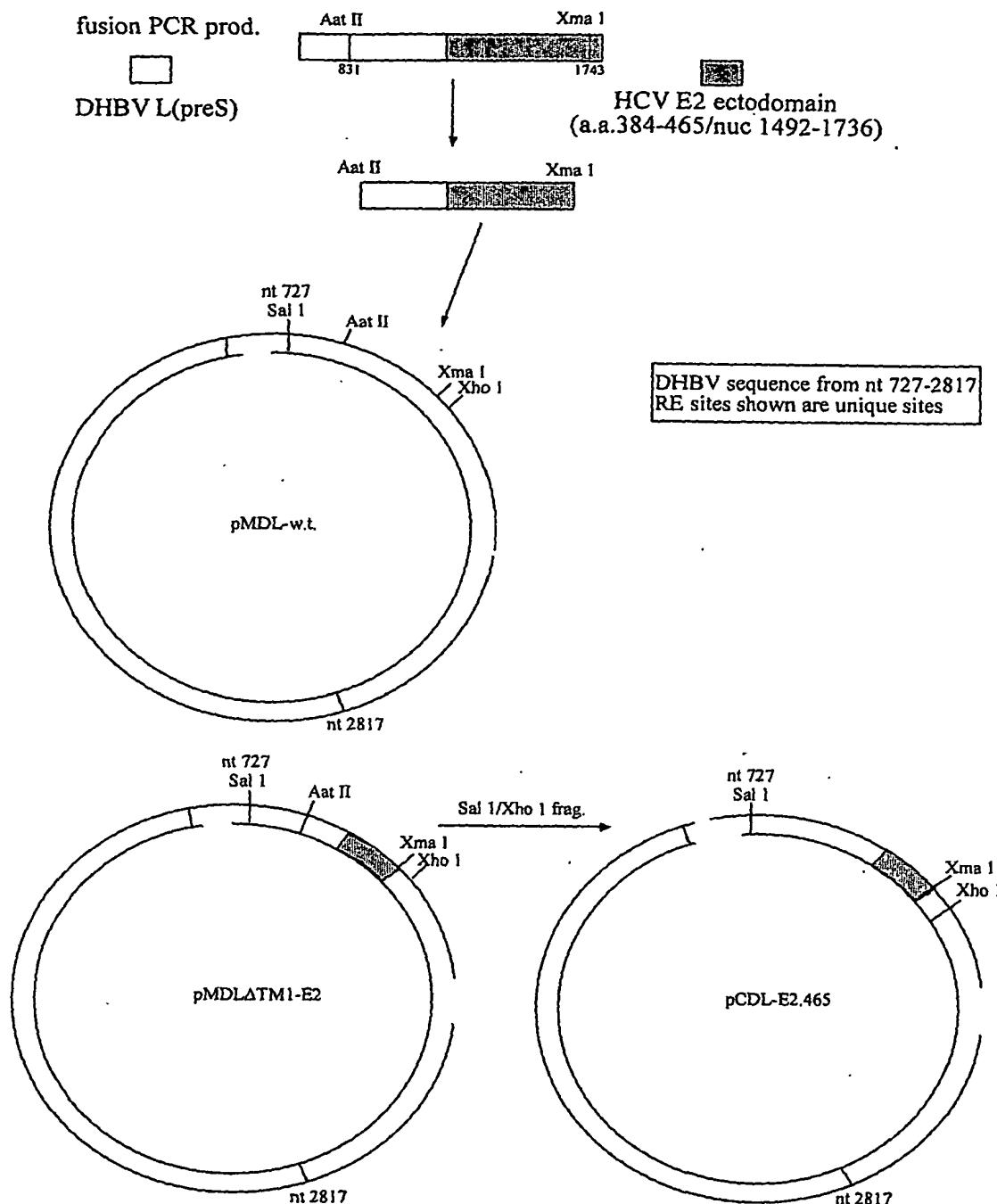
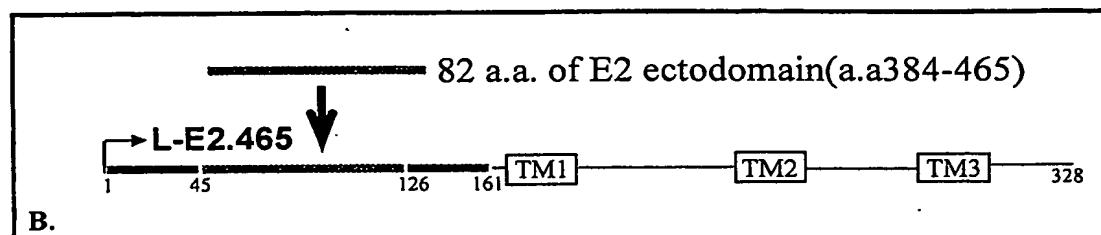
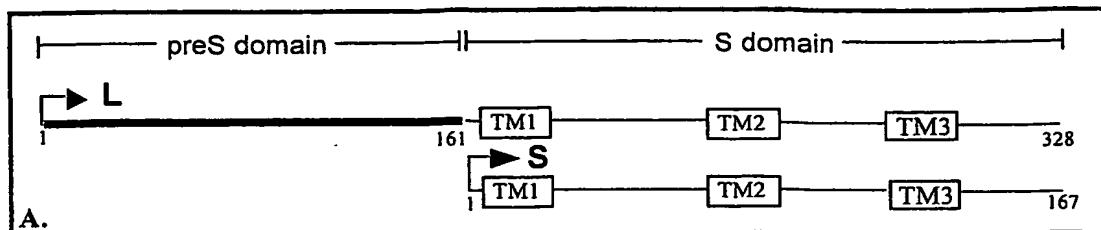


FIGURE 1

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C. L-E2.465 chimera is translocated across the ER membrane

trypsin	-	+	+
NP-40	-	-	+

L-E2.465 — — —

D. L-E2.465 chimera is assembled into particles

L-E2.465 — — —

S —

microsomes:protease protection assay

S —

particles purified by sedimentation through 20% sucrose

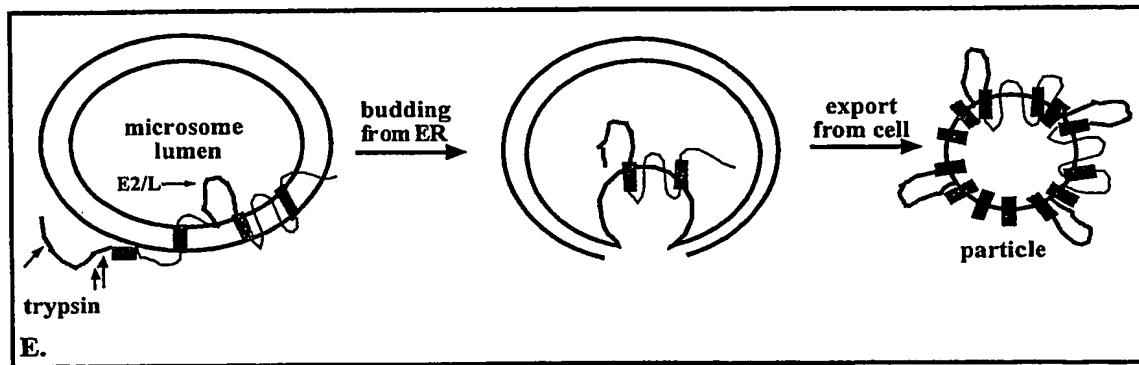


FIGURE 2

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DHBV full genome sequence (US D16 Acc. No. K01839)

1 catgctcatt tgaaagctta tgcaaaaatt aacgaggaat cactggatag ggcttaggaga
 61 ttgccttgggt ggcattacaa ctgttactg tggggagaag ctcaagttac taactatatt
 121 ttcgtttgc gtacttgggt gtcaactcct gagaaatata gagtagaga tgcccccacc
 181 attgaagcaa tcactagacc aatccaggtg gctcaggag gcagaaaaac aactacgggt
 241 actagaaaac ctcgtggact cgaacctaga agaagaaaag taaaaccac agttgtctat
 301 gggagaagac gttcaagtc ccgggaaagg agagcccta caccacaacg tgccggctcc
 361 cctctccac gtagttcgag cagccaccat agatctccct cgcttaggaa ataaattacc
 421 tgcttaggcat cacittagta aattgtcagg actatatcaa atgaaggcgt gtactttaa
 481 cccagaatgg aaagtaccag atattcggta factcattt aatttagatg tagttatga
 541 gtgccctcc cgaaatttga aatattgac tccagccaaa ttctggccca agagcatttc
 601 ctactttcct gtccaggtag gggtaaacc aaagtatcct gacaatgtga tgcaacatga
 661 atcaatagta ggtaaatatt taaccaggct ctatgaagca ggaatcctt ataagcggat
 721 atctaaacat ttggtcacat taaaaggta gccttataat tgggaacagc aacaccctgt
 781 caatcaacat cacattatg atggggcaac atccagcaaa atcaatggac gtcagacgga
 841 tagaaggagg agaaatactg taaaaccaac ttgccggaag gatgatccca aaagggactt
 901 tgacatggc aggcaagttt ccaacactag atcacgtgtt agaccatgtg caaacaatgg
 961 aggagataaa caccctccag aatcagggag ctggcctgc tggggcggga aggagagtag
 1021 gattatcaaa tccgactcct caagagattc ctcagccca gtggactccc gaggaagacc
 1081 aaaaagcacg cgaagctttt cggcggttacc aagaagaaaag accaccggaa accaccacca
 1141 ttccctcgtc ttccctcct cagtggaagc tacaaccgg ggacgatcca ctccctggaa
 1201 atcagtctct ctcgagact catccgctat accagttaga accagcggtg ccagtgataa
 1261 aaactccccctt ctgaagaag aaaatgtctg gtaccttcgg gggaaatacta gctggcctaa
 1321 tcggattact ggtaagcttt ttcttgtga taaaattct agaaatactg aggaggctag
 1381 atttgtggtg gatttcttc agtttccaa agggaaaaat gcaatgcgt ttccaagata
 1441 ctggagccca aatcttcca cattacgttag gatcttgcctt gtggggatgc ccaggatttc
 1501 ttggaccta ttcaggctt ttatcatct tcctcttaat cctgctagta gcagcaggct
 1561 tgctgtatct gacggacaac gggctacta ttttagaaaa gctcaatgg gcgtcggtt
 1621 cagccctttt ctccctccatc tcttcaactac tggccctcgg tccgaaatct ctgcgtcgctt
 1681 taacgtttgg actttcaattt atatggatga ctccctcctc tgccacccaa acgctcgta
 1741 ccttaacgca attagccacg ctgtcgctc tttttacaa gagtttaggaa taagaataaa
 1801 cttgacaaa accacgcctt ctccggtaa tggaaataaga ttccctgggtt accagatgt
 1861 tgaaaatttc atgaagattg aagaagcag atggaaagaa ttaaggactg taatcaagaa
 1921 aataaaagta ggagaatggt atgactggaa atgtattcaa agatttgtgg ggcatttgaa
 1981 ttttgttttg ctcttacta aaggtatat tggaaatgtta aaaccaatgt atgctgctat
 2041 tactaaccaa gtaaacttta gcttccttc atcctatagg actttgttat ataaactaac
 2101 aatgggtgtg tggtaattaa gaataaagcc aaagtccctt gtacctttgc cacgtgtac

FIGURE 3

2161 tacagatgt accccaacac atggcgcaat atcccatatc accggcggga gcgcagtgt
2221 tgctttca aaggtcagag atatacatgt tcaggaacta ttgatgtctt gtttagccaa
2281 gataatgatt aaaccacgtt gtctcttatac tgattcaact ttgtttgccc ataagcgta
2341 tcagacgtt ccatggcatt ttgctatgtt gccaaacaa ttgctcaaac cgataacaatt
2401 gtactttgtc cgagcaaataaataatcctgc tgacggccca tccaggcaca aacctcctga
2461 ttggacggct ttccatatac cccctcttc gaaagcaata tatattccac ataggctatg
2521 tggaaacttaa gaattacacc ccttccttc ggagctgtt gccaaggatcttacgtct
2581 acattgttgt tgcgtgtgt gactgtaccc ttggatgtta ccattgtta tgattctgc
2641 ttatatatgg atatcaatgc ttcttagagcc ttgcataatg tgcgtatgtt accagatgtat
2701 ttcttccaa aaatagatga tcttgttaga gatgctaaag acgctttaga gccttattgg
2761 aaatcagatt caataaagaa acatgttttgc attgcaactc actgtgtgg tctcattgaa
2821 gacttctggc agactacaca gggcatgcat gaaatagccg aatcattaag agctgttata
2881 cctccacta ctactcctgt tccaccgggt tatcttattc acgacgagggaa agctgaagag
2941 ataccccttgg gagatttatt taaacacccaa gaagaaagggaa tagtaagttt ccaacccgac
3001 tatccgattt ccggcttagaaat t

FIGURE 3 Cont.

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DHBV L sequence (US D16) (start L atg 801; start S atg 1284)

801/1	atg	ggg	caa	cat	cca	gca	aaa	tca	atg	gac	gtc	aga	cgg	ata	gaa	ggg	gaa	ata	ctg		
M	G	Q	H	P	A	K	S	M	D	V	R	I	E	G	G	E	I	L			
861/21	tta	aac	caa	ctt	gcc	gga	agg	atg	atc	cca	aaa	ggg	act	ttg	aca	tgg	tca	ggc	aag	ttt	
L	N	Q	L	A	G	R	M	I	P	K	G	T	L	T	W	S	G	K	F		
921/41	cca	aca	cta	gat	cac	gtg	tta	gac	cat	gtg	caa	aca	atg	gag	gag	ata	aac	acc	ctc	cag	
P	T	L	D	H	V	L	D	H	V	Q	T	M	E	E	I	N	T	I	Q		
981/61	aat	cag	gga	gct	tgg	cct	gct	ggg	gca	ggg	gga	agg	aga	gta	gga	tta	tca	aat	ccg	act	cct
N	Q	G	A	W	P	A	G	A	G	R	R	V	G	L	S	N	P	T	P		
1041/81	caa	gag	att	cct	cag	ccc	cag	tgg	act	ccc	gag	gaa	gac	caa	aaa	gca	cgc	gaa	gct	ttt	
Q	E	I	P	Q	P	Q	W	T	P	E	E	D	Q	K	A	R	E	A	F		
1101/101	cgc	cgt	tat	caa	gaa	aga	cca	ccg	gaa	acc	acc	acc	att	cct	ccg	tct	tcc	cct	cct		
R	R	Y	Q	E	R	P	P	E	T	T	T	I	P	P	S	S	P	P			
1161/121	cag	tgg	aag	cta	caa	ccc	ggg	gac	gat	cca	ctc	ctg	gga	aat	cag	tct	ctc	ctc	gag	act	
Q	W	K	L	Q	P	G	D	D	P	L	L	G	N	Q	S	L	L	E	T		
1221/141																					
1251/151																					

FIGURE 4

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cat ccg cta tac cag tca gaa cca gcg gtg cca gtg ata aaa act ccc ccc ttg aag aag	H P L Y Q S E P A V	V I	T K	P P L	K K
1281/161					
aaa <u>atg</u> tct ggt acc ttc ggg gga ata cta gct ggc cta atc gga tta ctg gta agc tt	K M S G T F G G	I I I A G L	I G I	G L V	S F
1341/181					
ttc ttg ttg ata aaa att cta gaa ata ctg agg cta gat tgg tgg att tct ctc	F L L I K I L E I	R R L D	W W W	I S L	
1401/201					
agt tct cca aag gga aaa atg caa tgc gct ttc caa gat act gga gcc caa atc tct cca	S S P K G K M Q C A F Q D T	G A Q G A	I S P		
1461/221					
cat tac gta gga tct tgc ccg tgg gga tgc cca gga tt ttt ttg acc tat ctc agg ctt	H Y V G S C P W G C	P G F	L W T	Y L R	L
1521/241					
ttt atc ttc ctc tta atc ctg cta gta gca gca ggc ttg ctg tat ctg acg gac aac	F I I F L L I L V A A G	L L Y L T	D N		
1581/261					
ggg tct act att tta gga aag ctc caa tgg gcg tgc tca gcc ctt ttc tcc ttca	G S T I L G K L Q W A S V	S A L F	S S I		
1641/281					
tct tca cta ctg ccc tcg gat ccg aaa tct ctc gct tta acg tt gga ctt tca tt	S S L L P S D P K S L V A L T F G L S L				
1701/301					
1731/311					
1491/231					
1551/251					
1611/271					
1671/291					

FIGURE 4 Cont.

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ata tgg atg act tcc tcc tct gcc acc caa acg ctc gtc acc tta acg caa tta gcc acg
I W M T S S Q T L V T Q L A T
1761/321 1791/331

ctg tct gct ctt ttt tac aag agt tag
L S A L F Y K S *

FIGURE 4 Cont.

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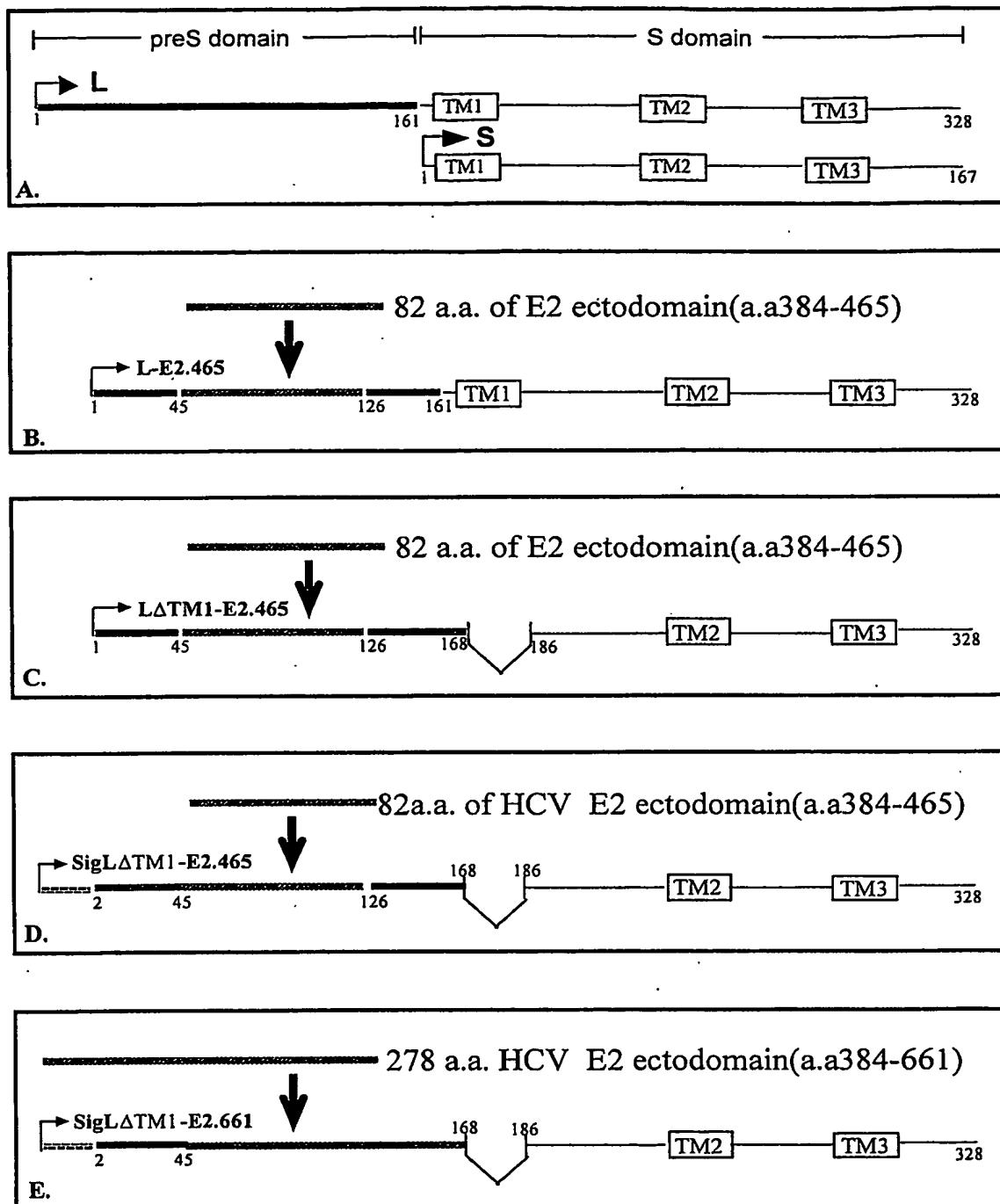
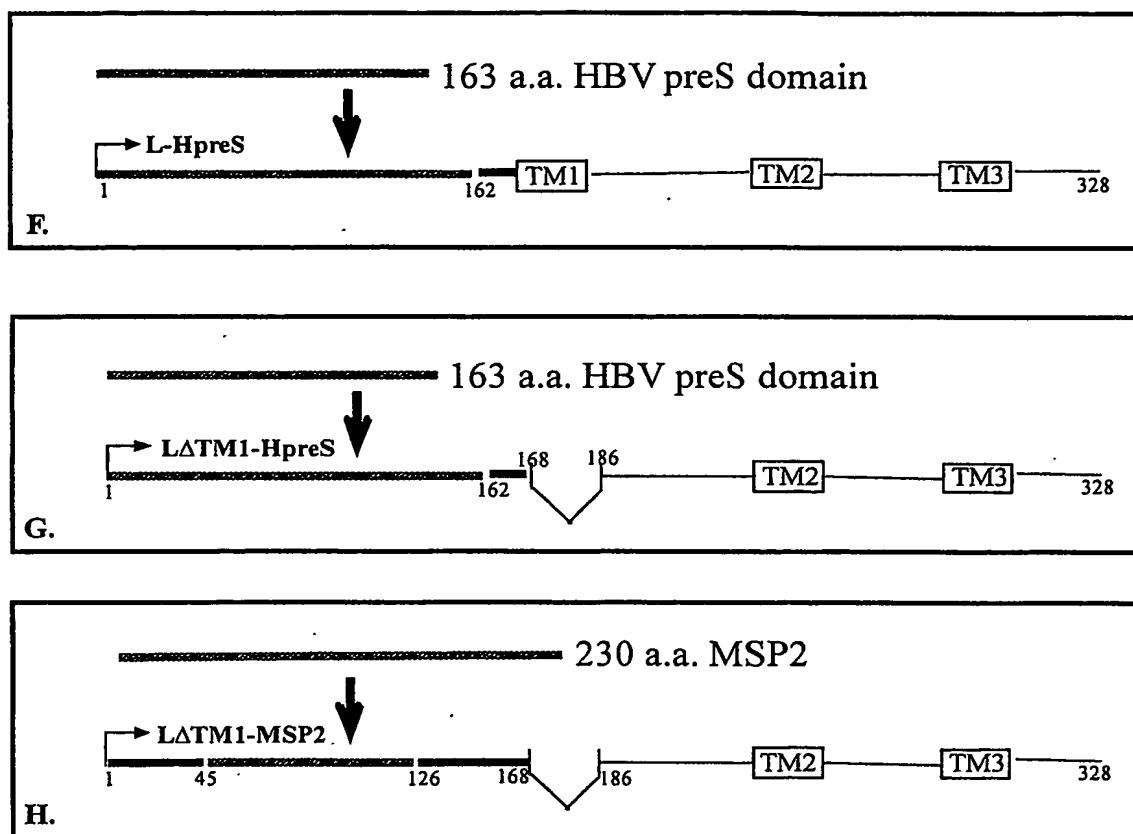
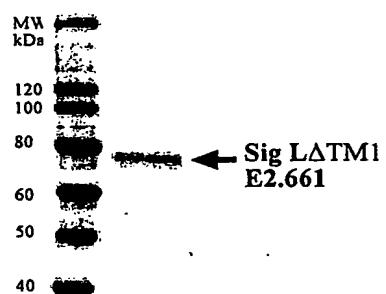
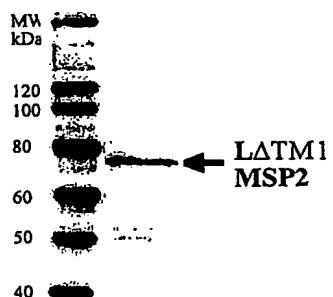


FIGURE 5

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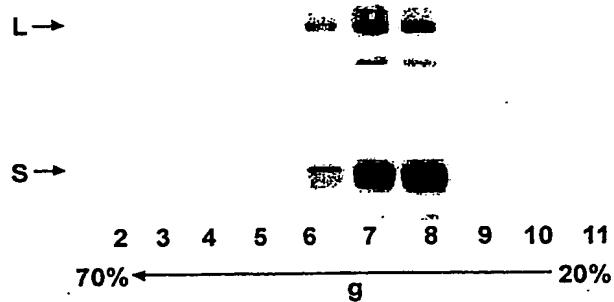
**FIGURE 5 cont.**

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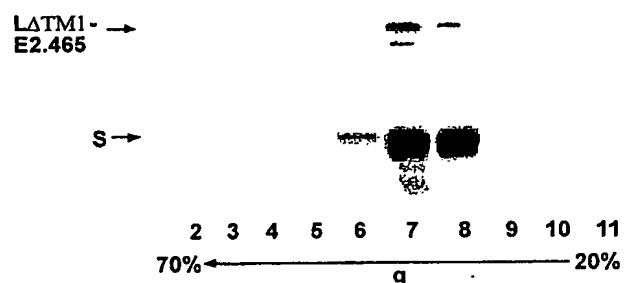
A. SigL Δ TM1-E2.661 membrane fraction**B. L Δ TM1-MSP2 membrane fraction****FIGURE 6**

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A. DL/S VLPs:sucrose step gradient profile



B. DLΔTM1-E2.465 VLPs: sucrose step gradient profile



C. DLΔTM1-HpreS VLPs: sucrose step gradient profile

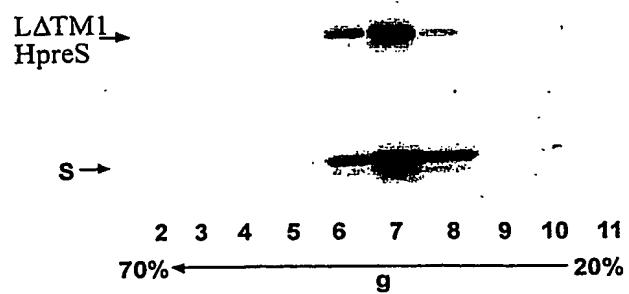
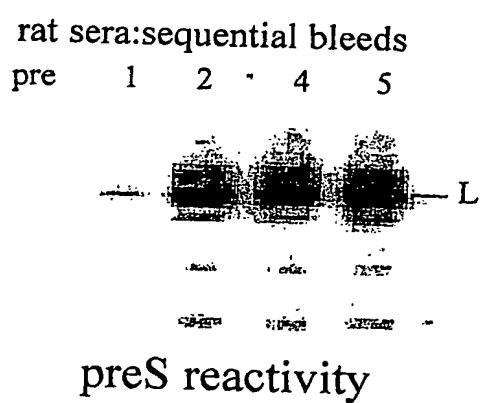


FIGURE 7

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**FIGURE 8**